Clean Copy of Second and Third full Paragraphs on Page 7

Fig. 4 [SEQ. ID NOs:5-17] (AP3, SEQ ID NO:5; DEFA, SEQ ID NO:5; AG_, SEQ ID NO:6; MCM1, SEQ ID NO:7; SRF, SEQ ID NO:8; GLO, SEQ ID NO:9; RLM1-yeast, SEQ ID NO:10; SMP1-yeast, SEQ ID NO:11; MEF2D, SEQ ID NO:12; AGL5, SEQ ID NO:13; FBP11, SEQ ID NO:14; BOAP1, SEQ ID NO:15; AGL11, SEQ ID NO:16; SPL, SEQ ID NO:17) illustrates the alignment of the first 18 amino acids of the MADS domains from several MADS box transcription factors with amino acids 64 to 80 of the SPL protein.

A1

Fig. 5 [SEQ. ID NO:18] shows the DNA sequence of the promoter of the *SPL* gene and the coding region of the gene. The promoter sequence begins 2690 nucleotides upstream of the start codon of the *SPL* gene. The first nucleotide of the start ATG codon is designated as position +1. The start codon ATG and the stop codon TAA are underlined, and two exons are shown in bold.

Clean Copy of Paragraph Bridging Pages 7 and 8:

As stated above, the present invention provides isolated nucleic acid molecules (e.g., DNA or RNA) that encode proteins which are involved in, and may be essential to, the formation of meiocytes in the male and female organs of plants. The nucleic acid molecules described herein are useful for producing *Sporocyteless* (SPL) proteins and SPL-type proteins of plant origin when such nucleic acids are incorporated into any of a variety of protein expression systems known to those skilled in the art. An isolated *SPL* gene in accordance with the present invention is shown in Figure 2 [SEQ ID NO:1]. The sequence of the promoter region of the *SPL* gene, as well as the coding region of the gene is shown in Figure 5 [SEQ. ID NO:18].

A2

Replace First Full Paragraph on Page 16 with the following:

There also is provided an isolated nucleic acid sequence or its complement or which hybridizes to said sequence which comprises the contiguous nucleotide sequence as set forth in Figure 2 [SEQ ID NO:1] or a portion thereof which is preceded by a nucleic acid sequence which provides the promoter region of the gene. A nucleotide sequence which provides the promoter region is shown in Figure 5 [SEQ ID NO:18]. Specifically, the promoter comprises the sequence located within nucleotide positions -2690 to -1 of the sequence set forth in Figure 5 [SEQ ID NO:18], or functional fragments thereof capable of regulating expression of an operably linked gene.

Replace Second Paragraph Bridging Pages 25 and 26 with the following:

Another embodiment of the invention provides an isolated promoter of the *SPL* gene. A fragment of DNA extending from 2690 nucleotides upstream of the start codon of the *SPL* gene has been identified as regulating expression of the *SPL* gene. The sequence of this promoter is shown in Figure 5 [SEQ. ID NO: 18] as the sequence from base pair -2690 to -1 in the sequence. The first nucleotide of the start ATG codon is designated as position +1 in the sequence. The sequence from -2690 to -1 is sufficient to give *SPL*-specific expression in megasporocytes and microsporocytes. As used herein, "promoter" includes this sequence, a sequence which hybridizes to this sequence and promotes expression of a coding sequence operably linked thereto, and functional fragments of this sequence which are capable of promoting or regulating expression of a coding sequence operably linked thereto. The promoter can be operably linked to a coding sequence if it is linked to the ATG start codon of the coding sequence.

Replace the Paragraphs Bridging Pages 31 and 32 with the following:

In addition, there is a predicted helix region in SPL protein from amino acids 64 to 85 that has limited homology with the first helix region of the protein motif called the MADS domain that binds DNA. The MADS domain is a highly conserved region of about 57 amino acids found in a family of transcription factors called MADS box factors (See, *e.g.*, Kramer et al., *Genetics* 149:765-783 (1998)). SPL does not have the entire MADS domain, but it shows good conservation to the first 18 amino acids of this domain. A comparison of amino acids 64 to 80 of SPL with the first amino acids of the MADS domain from known regulatory proteins of this class from a variety of species is shown in Figure 4 [SEQ ID NOS:5-17].

Replace the First Full Paragraph on Page 32 with the following:

As shown in Figure 4 [SEQ ID NOS:5-17], the MADS box transcription factors listed are the AP3, AG, AGL5 and AGL11 proteins of Arabidopsis; DEFA and GLO proteins of Antirrhinum (snapdragon); BOAP1 from Brassica oleracea; FBP11 from petunia; MCM1, RLM1, SMP1 proteins from budding yeast; and SRF and MEF2D human proteins.

Replace the Paragraph Bridging Pages 41 and 42 with the following:

Two primers, SPL-Xba-S:5'CTAGTCTAGTCTAGAAGATCATCA3' [SEQ ID NO:19] and SPL-BamH1-T:5'CGGATCCAAGCTTCAAGGACAAATCAATGGT3' [SEQ ID NO:20], which introduced restriction enzyme sites immediately upstream of the *SPL* start codon and the *SPL* stop codon, respectively, were used to amplify the complete *SPL* coding sequence from the cDNA. This amplified fragment was cloned in front of the GUS gene in the pBI221 vector (Clontech), giving rise to clone pBI221-SPL, which encodes a SPL-GUS fusion. The gene fusion in pBI221-SPL is driven by the 35S promoter and will result in the synthesis in plant cells of a fusion protein consisting of the complete SPL protein at the N terminus and the GUS protein at the C terminus.

Clean Copy of Amended Claims

45. (Amended) An isolated nucleic acid sequence comprising a nucleic acid sequence as set forth in nucleotides -2690 to -1 of SEQ ID NO:18 or a nucleotide sequence which hybridizes to said sequence and promotes expression of a coding sequence operably linked to said nucleotide sequence.

(AMENDED)
46. An isolated nucleotide sequence or functional fragments thereof capable of regulating expression of an operably linked gene, said sequence comprising a nucleotide sequence located within nucleotide positions -2690 to -1 of the nucleotide sequence set forth in SEQ ID NO:18 or a nucleotide sequence which hybridizes to said sequence and promotes expression of an operably linked gene.